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1 TENPCAQRCLQSCQQEPDDL.....
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O27383 caenorhabdi
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ALIGNMENTS

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                    Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson
Craxton M., Dear S., Du Z., Durbin R., Favello, A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.
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Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 M of contiguous nucleotide sequence from chromosome III of C
                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE-94150718; PubMed-7906398;
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Caenorhabditis elegans.
                                                                                                                                                                                                                                                                Rhabditidae; Pel
NCBI_TaxID=6239;
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Rhabditidae; Peloderinae;
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
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Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
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                                                                                                                                                                                                                                                                                   Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.; "2.2 Mb of contiguous nucleotide sequence from chromosome II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
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Rhabditidae; Peloderinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1997) to the AAB94214.1;
                                                                                                                                                                   Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nematoda; Chromadorea; rinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41440 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.8%;
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                                                                                                                                            the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bauer C.,
                                                                                                                                              EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        emat/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EA9C34AA4EABFE46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence
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J databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
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Best Local
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                     Submitted (JUL-1996) to the EM-
-! SIMILARITY: BELONGS TO FAM
EMBL; U64859; AAC69090.1; -.
EMBL; U64859; AAC69096.1; -.
WORMPEP; R09F10.2; CE07436.
WORMPEP; R09F10.7; CE07441.
                       EMBL; AF1
HSSP; P02
INTERPRO;
                              globulin protein in Macadamia integrifolia. Plant J. 0:0-0(1999). EMBL: APIG1885; AAD54246 1. HSSP; PO2853
       PFAM; PF
                                                                                                            Macadamia integrifolia (Macadamia nut).
Macadamia integrifolia (Macadamia nut).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 06, Last annotation update)
HYPOTHETICAL 40.7 KDA PROTEIN R09F10.2 IN CHROMOSOME
R09F10.2 AND R09F10.7.
                                                                                                                                                       01-MAY-2000
01-OCT-2000
                                                                                                                                                                        Q9SPL3;
01-MAY-2000
                                                                                                                                                                                         Q9SPL3
                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
 SEQUENCE
                                                                                       SEQUENCE FROM N.A.
                                                                                                        NCBI_TaxID=60698;
                                                                                                                                               VICILIN PRECURSOR
                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                       Hypothetical protein; Signal. SIGNAL 1 18
                                                                                                                                                                                                                                                                                                                                                                                       Couch J
                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q27383
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                                                                                                                                                                                                                                 84
                                                                                                                                                                                                                                                               Local Similarity 37.8 les 14; Conservative
                                                                                                                                                                                                                              ω
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                PF00546; Seedstore_7s;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
                        IPR001113;
625
                                                                                                                                                                                                                                                                                                        19
378 AA;
                                                                                                                                                      (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY
ΑA;
                                                                                                                                               (FRAGMENT).
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378 H
40683 MW;
73586 MW;
                                                                                                                                                                                                                                                                       20.4%;
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                                                                                                                                                                                                                                                                                                                                                                       the EMBL/GenBank/DDBJ databases TO FAMILY UPF.
                                                                                                                                                                                                                                                               Score 70; DB Pred. No. 0.6; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 70; DB 5; Pred. No. 0.37; 7; Mismatches
                                                                                                                                                                                                                                                                                                        HYPOTHETICAL PROTEIN R09F10; E58B416BFE3A7610 CRC64;
                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
415808A89D370296 CRC64;
                                                                                                                                                                                       625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       378
                                                              Manners J.M.
produced by
                                                                                                                                                                                                                                                                     о.6;
                                                                                                                                                                                       AA
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                                                                                                                                                                                                                                                                              Length 378
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                                                                                                                                                                                                                                                               Indels
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                                                               processing
                                                                                                                      Spermatophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhabditoidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
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                                                                                                                                                                                                                                                               6;
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                                                               of 'a
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Q49549
       29
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Best Local :
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                                                                                                                                       AMP2
                                                                                                                                                                                                                               461
                                                                                                                                                                                                                                                               403
                                                                                                                                                                                                                                              47
                                                                                                                                                                                                                                                                              8
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Best Local Similarity Matches , 12; Conserv
                                                                                                                                                                                                                                                                                                    Q9SPL4
Q9SPL4;
01-MAY-2000
01-MAY-2000
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q49549;
Q49549;
01-NOV-1996
                                               globulin protein in Macadamia Plant J. 0:0-0(1999). EMBL; AF161884; AAD54245.1; -. HSSP; P02853; 2PHL.
                                                                                                                                                                                                               Macadamia integrifolia (Macadamia nut).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Maαπολίουhvta: eudicotyledons; Proteaceae; Macadamia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
REPEAT REGIONS IN POTENTIAL METAL BINDING PROTEIN GENE REGION
Mycoplasma hyorhinis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Mycoplasma.
                                                                                                               TISSUE=NUT KERNEL;
Marcus J.P., Goulter K.C.,
"A family of antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Deng G., McIntosh M.A.;

"An amplifiable DNA region from the J. Bacteriol. 176:5929-5937(1994).

EMBL; L11447; AAA62228.1; -.

SEQUENCE 1187 AA; 135027 MW; 66A
                                                                                                                                                                                                                                                                                      VICILIN PRECURSOR.
                   PFAM; PF00546;
                                 INTERPRO; IPR001113; -
                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                   NCBI_TaxID=60698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95014025; PubMed=7928953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=GDL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=2100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 CORRCKEICEEEEEYNRQRDPQQQYEQCQKRCQRRETEPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 CAQRCLQSCQQEPDDLKQK-----ACESRCTKLEYDPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TEEHC--ECTESTCGCENEPCECEEEACDCSEEHCECVDETQACLDCNTQADTKVCGCTQ 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQHPTCEECK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                   (TremBLrel. 13, Created)
(TremBLrel. 13, Last sequ
(TremBLrel. 15, Last anno
                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
Seedstore_7s;
AA; 78243 MW;
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                                                                                                                 Green J.L.,
peptides is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 69; DB
Pred. No. 2.2;
l2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 69.5;
Pred. No. 1
                                                                                              een J.L., Manners of ptides is produced integrifolia.";
                                                                                                                                                                                                                                                                                                                                                                        PRT;
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0ECA22F8710F8A7B CRC64;
                                                                                                                                                                                                                                                                                                    sequence up
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                                                                                                                 processing
                                                                                                                                                                                                                                  Spermatophyta;
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                                                                                                                   of
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RESULT
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01-JAN-1998
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Bonfield J., Burton J., Connell M., Copsey T., Coulson A.,
Craxton M., Dear S., Du 2., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
7.2 Mb of contiguous nucleotide sequence from chromosome III of C.
SEQUENCE FROM N.A. STRAIN=BRISTOL N2:
                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 01-NOV-1998 (TrEMBLrel.
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01-JAN-1998 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
                                                                                          Rhabditidae; Peloderinae; NCBI_TaxID=6239;
                                                                                                                                Eukaryota; Metazoa;
Rhabditidae; Pelodei
                                                                                                                                                                                       Caenorhabditis elegans
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EMBL; Z81573; CAB04625.1; -.
HSSP; O46655; 1CJH.
SEQUENCE 1513 AA; 161578;
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| :|| :| :| :| :| :| | :|| :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
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Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
"2.2 M. of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                            Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson of Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
                                                SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
Eukaryota; Metazoa; Nen
Rhabditidae; Peloderina
NCBI_TaxID=6239;
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Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases
EMBL; AF016451; AAB65995.1; -.
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STRAIN-BRISTOL N2;
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STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                     MEDLINE=94150718; PubMed=7906398;
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.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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                                                                                                  368:32-38(1994).
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                 (AUG-1997) to the EMBL/GenBank/DDBJ databases
                                Bradshaw H.,
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                                  Elliott G.;
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O19919 PRELIMINARY; PRT; 242 AA. Q19919; O1-JUN-1998 (TrEMBLrel. 06, Created) O1-JUN-1998 (TrEMBLrel. 06, Last sequence update) O1-JUN-1998 (TrEMBLrel. 06, Last annotation update) HYPOTHETICAL 26.2 KDA PROTEIN F31A3.1 IN CHROMOSOME F31A3.1.
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SEQUENCE
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EMBL; ACOU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
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01-JUN-2000 (TrEMBLrel. 14, Last ann
SEMAPHORIN III PRECURSOR (FRAGMENT).
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Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases
EMBL; AF016451; AAB66007.1; -
SEQUENCE 445 AA; 48282 MW; A65C08DC136BBADA CRC64;
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STRAIN=BRISTOL N2;
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MEDLINE=99063792; PubMed=9847074;
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01-MAY-2000
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Catarrhini;
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STRAIN-BRISTOL NZ;

MUTRAY J., Le T.T.;

Submitted (MAY-1996) to the EMBL/GenBank/DDBJ data to the EMBL, GenBank/DDBJ data to the EMBL; UPF.

EMBL; US8742; AAB36856.1; -.

ROMRMPEP; F31A3.1; CE071158.

WORMPEP; F31A3.1; CE07158.

HYPOTHETICAL PROTECTION: Transmembrane.

TRANSMEM

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SEQUENCE 242 AA; 26213 MW; C7D6996BD0829317 C
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016500;
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01-JAN-1998
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson /
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Latster N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vandhan P.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C
                                                            Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases EMBL; AF016451; AAB66001.1; . SEQUENCE 388 AA; 42139 MW; 2E20655B0B9AE492 CRC64;
                                                                                                             SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
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MEDLINE=94150718; PubMed=7906398;
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Rhabditidae; Pelode
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Rhabditidae;
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e; Peloderinae; Caenorhabditis.
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o the EMBL/GenBank/DDBJ databases
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Caenorhabditis.
  4.
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 Score 66; DB Pred. No. 1.9; 4; Mismatches
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; C7D6996BD0829317 CRC64;
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O16501;
O1-501-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
O1-MOV-1998 (TrEMBLrel. 08, Last annotation update)
CO3A7.7 PROTEIN.
CO3A7.7. PROTEIN.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID-6239;
                                                                                                                                                                                                                 Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases EMBL; AF016451; AAB65996.1; -. SEQUENCE 388 AA; 42129 MW; 74ACA3953E0AF2A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hiller L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
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Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=BRISTOL N2; Waterston R.;
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Greco T., Bradshaw H., Elliott G.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-BRISTOL N2,
MEDLINE-94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                          Nature 368:32-38(1994).
[2]
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43.8%;
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